

#3



SEQUENCE LISTING

RECEIVED
OCT 09 2001
TECH CENTER 1600/2900

<110> Sinds, Jack R.
de la Monte, Suzanne M.
Ince, Nedim
Carlson, Rolf I.

<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 DIV2

<140> 09/903,216

<141> 2001-07-11

<150> 09/436,184

<151> 1999-11-08

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
EGF-like domain

<220>

<221> VARIANT

<222> (2)..(8)

<223> Wherein Xaa is any amino acid

<220>

<221> VARIANT

<222> (10)..(13)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (15)..(24)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (26)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

<400> 1

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Cys
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser
1 5 10 15

Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
20 25 30

Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
115 120 125

Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
 130 135 140

Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
 145 150 155 160

Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
 165 170 175

Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
 180 185 190

Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
 195 200 205

Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
 210 215 220

Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
 225 230 235 240

Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
 245 250 255

Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
 260 265 270

Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
 275 280 285

Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
 290 295 300

Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
 305 310 315 320

Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
 325 330 335

Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
 340 345 350

Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val
 355 360 365

Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
 370 375 380

Glu	Asp	Asp	Leu	Ala	Glu	Lys	Arg	Arg	Ser	Asn	Glu	Val	Leu	Arg	Gly	385	390	395	400
Ala	Ile	Glu	Thr	Tyr	Gln	Glu	Val	Ala	Ser	Leu	Pro	Asp	Val	Pro	Ala	405	410	415	
Asp	Leu	Leu	Lys	Leu	Ser	Leu	Lys	Arg	Arg	Ser	Asp	Arg	Gln	Gln	Phe	420	425	430	
Leu	Gly	His	Met	Arg	Gly	Ser	Leu	Leu	Thr	Leu	Gln	Arg	Leu	Val	Gln	435	440	445	
Leu	Phe	Pro	Asn	Asp	Thr	Ser	Leu	Lys	Asn	Asp	Leu	Gly	Val	Gly	Tyr	450	455	460	
Leu	Leu	Ile	Gly	Asp	Asn	Asp	Asn	Ala	Lys	Lys	Val	Tyr	Glu	Glu	Val	465	470	475	480
Leu	Ser	Val	Thr	Pro	Asn	Asp	Gly	Phe	Ala	Lys	Val	His	Tyr	Gly	Phe	485	490	495	
Ile	Leu	Lys	Ala	Gln	Asn	Lys	Ile	Ala	Glu	Ser	Ile	Pro	Tyr	Leu	Lys	500	505	510	
Glu	Gly	Ile	Glu	Ser	Gly	Asp	Pro	Gly	Thr	Asp	Asp	Gly	Arg	Phe	Tyr	515	520	525	
Phe	His	Leu	Gly	Asp	Ala	Met	Gln	Arg	Val	Gly	Asn	Lys	Glu	Ala	Tyr	530	535	540	
Lys	Trp	Tyr	Glu	Leu	Gly	His	Lys	Arg	Gly	His	Phe	Ala	Ser	Val	Trp	545	550	555	560
Gln	Arg	Ser	Leu	Tyr	Asn	Val	Asn	Gly	Leu	Lys	Ala	Gln	Pro	Trp	Trp	565	570	575	
Thr	Pro	Lys	Glu	Thr	Gly	Tyr	Thr	Glu	Leu	Val	Lys	Ser	Leu	Glu	Arg	580	585	590	
Asn	Trp	Lys	Leu	Ile	Arg	Asp	Glu	Gly	Leu	Ala	Val	Met	Asp	Lys	Ala	595	600	605	
Lys	Gly	Leu	Phe	Leu	Pro	Glu	Asp	Glu	Asn	Leu	Arg	Glu	Lys	Gly	Asp	610	615	620	
Trp	Ser	Gln	Phe	Thr	Leu	Trp	Gln	Gln	Gly	Arg	Arg	Asn	Glu	Asn	Ala	625	630	635	640

Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu
645 650 655

Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro
660 665 670

Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg
675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
690 695 700

Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp
705 710 715 720

Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
725 730 735

Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
740 745 750

Arg Ser Leu Pro Ala Ile
755

<210> 3

<211> 2324

<212> DNA

<213> Homo sapiens

<400> 3

cggaccgtgc aatggccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60
gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccg agagagacaa 120
agcatggagg acacaagaat gggaggaaag gcggactctc gggaacttca ttcttcacgt 180
ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcggt tggtttgatc 240
ttgttgacta tgaggaagtt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300
atthttagtg ggatgatgcc aaagtthtat taggacttaa agagagatct acttcagagc 360
cagcagtccc gccagaagag gctgagccac aactgagcc cgaggagcag gttcctgtgg 420
aggcagaacc ccagaatatt gaagatgaag caaaagaaca aattcagtc cttctccatg 480
aatggtaca cgcagaacat gttgaggag aagacttgca acaagaagat ggaccacag 540
gagaaccaca acaagaggat gatgagttt ttatggcgac tgatgtagat gatagatttg 600
agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660
cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720
attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780
accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaagg atagaaatca 840
cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900
aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960
cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1020

```

ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaatgagg 1200
tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1260
acctgctgaa gctgagtttg aagcgctcgt cagacaggca acaatttcta ggatcatatga 1320
gaggttccct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
aaaatgacct tggcggtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1440
atgaagaggt gctgagtgtg acacctaata atggctttgc taaagtccat tatggcttca 1500
tcctgaaggc acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1560
ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1620
gggttgggaa caaagaggca tataagtggg atgagcttgg gcacaagaga ggacactttg 1680
catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttggtgga 1740
cccaaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaaagttaa 1800
tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1860
aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1920
atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1980
caacaggatg cagaagagga cagatcaaat attccatcat gcaccccgag actcacgtgt 2040
ggcgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaagggtg 2160
tcatctttga tgactccttt gagcacgagg tatggcagga tgcctcatct ttccggctga 2220
tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
caatttagca tgaattcatg caagcttggg aaactctgga gaga 2324

```

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-like
cysteine-rich repeat

<220>

<221> VARIANT

<222> (3)..(5)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (6)..(7)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> Wherein Xaa is any amino acid.

<220>
 <221> VARIANT
 <222> (14)
 <223> Wherein Xaa is any amino acid.

<220>
 <221> VARIANT
 <222> (17)..(18)

<220>
 <221> VARIANT
 <222> (25)..(26)
 <223> Wherein Xaa is any amino acid.

<220>
 <221> VARIANT
 <222> (29)
 <223> Wherein Xaa is any amino acid.

<400> 4
 Cys Asp Xaa Xaa Xaa Cys Xaa Xaa Lys Xaa Gly Asn Gly Xaa Cys Asp
 1 5 10 15
 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
 20 25 30

<210> 5
 <211> 1242
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val
 1 5 10 15
 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
 20 25 30
 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
 35 40 45
 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
 50 55 60
 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
 65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
 85 90 95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
 100 105 110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
 115 120 125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
 130 135 140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
 145 150 155 160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
 165 170 175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
 180 185 190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
 195 200 205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
 210 215 220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
 225 230 235 240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
 245 250 255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
 260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
 275 280 285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
 290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
 305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
 325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
 340 345 350
 Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
 355 360 365
 Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
 370 375 380
 Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Ser Thr Ser Gly His
 385 390 395 400
 Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
 405 410 415
 Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly
 420 425 430
 Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp
 435 440 445
 Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn
 450 455 460
 Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn
 465 470 475 480
 Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro
 485 490 495
 Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala
 500 505 510
 Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala
 515 520 525
 Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser
 530 535 540
 Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro
 545 550 555 560
 Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe
 565 570 575
 Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu
 580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr
 595 600 605

Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser
 610 615 620

Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val
 625 630 635 640

Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg
 645 650 655

Val Asp Pro Asn Gly Tyr Met Met Met Ser Pro Ser Gly Gly Cys Ser
 660 665 670

Pro Asp Ile Gly Gly Gly Pro Ser Ser Ser Ser Ser Ser Ser Asn Ala
 675 680 685

Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly
 690 695 700

Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser
 705 710 715 720

Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser
 725 730 735

Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly
 740 745 750

Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro
 755 760 765

Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala
 770 775 780

Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr
 785 790 795 800

Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu
 805 810 815

Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro
 820 825 830

His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala
 835 840 845

Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly
 850 855 860

Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln
 865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr
 885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro
 900 905 910

Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln
 915 920 925

Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met
 930 935 940

Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val
 945 950 955 960

Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys
 965 970 975

Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met
 980 985 990

Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala
 995 1000 1005

Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu Val
 1010 1015 1020

Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser Ala Ala
 1025 1030 1035 1040

Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu Ala Ala His
 1045 1050 1055

Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly Met Ser Ala Phe
 1060 1065 1070

Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln Ser Ala Lys Val Ile
 1075 1080 1085

Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg His Ser Ser Glu Thr Phe
 1090 1095 1100

Ser Ser Thr Pro Ser Ala Thr Arg Val Gly Asn Thr Val Pro Phe Gly
 1105 1110 1115 1120

Ala Gly Ala Ala Val Gly Gly Gly Gly Ser Ser Ser Ser Ser Glu
 1125 1130 1135

Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg
 1140 1145 1150

Pro Gly Glu Leu Gly Gly Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly
 1155 1160 1165

Ala Ala Gly Gly Leu Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu
 1170 1175 1180

Val Lys Asp Phe Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln
 1185 1190 1195 1200

Pro Pro Pro Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser
 1205 1210 1215

Ser Ser Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile
 1220 1225 1230

Ser Phe Gln Lys Gln Pro Glu Asp Arg Gln
 1235 1240

<210> 6
 <211> 5828
 <212> DNA
 <213> Homo sapiens

<400> 6
 cggcggcgcg gtcggagggg gccggcgcgc agagccagac gccgccgctt gttttggttg 60
 gggctctcgg caactctccg aggaggagga ggaggaggga ggaggggaga agtaactgca 120
 gcggcagcgc cctcccgagg aacaggcgctc ttccccgaac ccttcccaaa cctcccccat 180
 cccctctcgc ccttgctccc tcccctcctc cccagccgcc tggagcgagg ggcaggggatg 240
 agtctgtccc tccggccggt cccagctgc agtggctgcc cggtatcggt tgcgatggaa 300
 aagccacttt ctccaccgc cgagatgggc ccgatgggg ctgcagagga cgcgcccgcg 360
 ggcggcggca gcagcagcag cagcagcagc agcaacagca acagccgcag cgcgcgggtc 420
 tctgcgactg agctggtatt tgggcggctg gtggcggctg ggacggttg ggggtgggag 480
 gaggcgaagg aggagggaga acccctgca acgttgggac ttggcaacc gcctccccct 540
 gcccaggat atttaatttg cctcgggaat cgctgcttcc agaggggaac tcaggaggga 600
 aggcgcgcgc gcgcgcgcgc tcttgaggg gcaccgcagg gacccccgac tgtcgcttcc 660
 ctgtgccgga ctccagccgg ggcgacgaga gatgcatctt cgctccttcc tgggtggcggc 720
 ggcggctgag aggagacttg gctctcggag gatcggggct gccctcacc cggacgcact 780
 gcctccccgc cggcgtgaag cggccgaaaa ctccggtcgg gctctctcct gggctcagca 840

gctgcgtcct	ccttcagctg	cccctccccg	gcgcgggggg	cggcgtggat	ttcagagtcg	900
gggtttctgc	tgcctccagc	cctgtttgca	tgtgccgggc	cgcggcgagg	agcctccgcc	960
ccccacccgg	ttgtttttcg	gagcctccct	ctgctcagcg	ttggtggtgg	cggtggcagc	1020
atggcgagcc	ctccggagag	cgatggcttc	tcgacgtgc	gcaaggtggg	ctacctgcgc	1080
aaacccaaga	gcatgcacaa	acgcttcttc	gtactgcgcg	cggccagcga	ggctgggggc	1140
ccggcgcgcc	tcgagtacta	cgagaacgag	aagaagtggc	ggcacaagtc	gagcgccccc	1200
aaacgctcga	tcccccttga	gagctgcttc	aacatcaaca	agcgggctga	ctccaagaac	1260
aagcacctgg	tggctctcta	cacccgggac	gagcactttg	ccatcgcggc	ggacagcgag	1320
gccgagcaag	acagctggta	ccaggctctc	ctacagctgc	acaaccgtgc	taaggggccac	1380
cacgacggag	ctgcggccct	cggggcggga	ggtggtgggg	gcagctgcag	cggcagctcc	1440
ggccttggtg	aggtggggga	ggacttgagc	tacggtgacg	tgcccccagg	acccgcattc	1500
aaagaggtct	ggcaagtgat	cctgaagccc	aagggcctgg	gtcagacaaa	gaacctgatt	1560
ggtatctacc	gcctttgcct	gaccagcaag	accatcagct	tcgtgaagct	gaactcggag	1620
gcagcgcccg	tgggtgctga	gctgatgaac	atcaggcgct	gtggccactc	ggaaaacttc	1680
ttcttcatcg	aggtggggcg	ttctgccgtg	acggggcccc	gggagttctg	gatgcagggtg	1740
gatgactctg	tgggtggccca	gaacatgcac	gagaccatcc	tggaggccat	gcggggccatg	1800
agtgatgagt	tccgcctctg	cagcaagagc	cagtcctcgt	ccaactgctc	taaccccatc	1860
agcgtccccc	tgcgcgggca	ccatctcaac	aatcccccg	ccagccaggt	ggggctgacc	1920
cgcgcgatcac	gcactgagag	catcacgcgc	acctccccg	ccagcatggt	gggcgggaag	1980
ccaggctcct	tccgtgtccg	cgctccagt	gacggcgaag	gcaccatgtc	ccgcccagcc	2040
tcggtggacg	gcagccctgt	gagtcccagc	accaacagaa	cccacgcca	ccggcatcgg	2100
ggcagcgccc	ggctgcaccc	cccgtcaac	cacagccgct	ccatccccat	gccggcttcc	2160
cgtctgctgc	cttcggccac	cagccgggtc	agtctgtcgt	ccagtagcac	cagtggccat	2220
ggctccacct	cggattgtct	cttcccacgg	cgatctagt	cttcggtgtc	tggttccccc	2280
agcgatggcg	gtttcatctc	ctcggatgag	tatggctcca	gtccctgcga	tttcgggagt	2340
tccttcgcga	gtgtcactcc	ggattccctg	ggccacaccc	caccagcccg	cggtgaggag	2400
gagctaagca	actatatctg	catgggtggc	aaggggccct	ccaccctgac	cgcccccaac	2460
ggtcactaca	ttttgtctcg	gggtggcaat	ggccaccgct	gcaccccagg	aacaggcttg	2520
ggcacgagtc	cagccttggc	tggggatgaa	gcagccagtg	ctgcagatct	ggataatcgg	2580
ttccgaaaga	gaactcactc	ggcaggcaca	tcccctacca	ttacccacca	gaagaccccg	2640
tcccagtcct	cagtggcttc	cattgaggag	tacacagaga	tgatgcctgc	ctacccacca	2700
ggaggtggca	gtggaggccg	actgccggga	cacaggcact	ccgccttcgt	gcccacccgc	2760
tcctacccag	aggagggtct	ggaaatgcac	cccttgagc	gtcggggggg	gcaccaccgc	2820
ccagacagct	ccaccctcca	cacggatgat	ggctacatgc	ccatgtcccc	aggggtggcc	2880
ccagtgccca	gtggccgaaa	gggcagtggg	gactatatgc	ccatgagccc	caagagcgta	2940
tctgccccac	agcagatcat	caatcccatc	agacgccatc	cccagagagt	ggaccccaat	3000
ggctacatga	tgatgtcccc	cagcgtggc	tgtctcctg	acattggagg	tggccccagc	3060
agcagcagca	gcagcagcaa	cgcgtccct	tccgggacca	gctatggaaa	gctgtggaca	3120
aacggggtag	ggggccacca	ctctcatgtc	ttgcctcacc	ccaaaccccc	agtggagagc	3180
agcgggtggt	agctcttacc	ttgcacaggt	gactacatga	acatgtcacc	agtgggggac	3240
tccaacacca	gcagcccctc	cgactgctac	tacggccctg	aggaccccca	gcacaagcca	3300
gtcctctcct	actactcatt	gccaagatcc	tttaagcaca	cccagcgccc	cggggagccg	3360
gaggaggggtg	cccgccatca	gcacctccgc	ctttccacta	gctctggtcg	ccttctctat	3420
gctgcaacag	cagatgattc	ttcctcttcc	accagcagcg	acagcctggg	tgggggatac	3480
tgcggggcta	ggctggagcc	cagccttcca	catccccacc	atcaggttct	gcagcccat	3540
ctgcctcgaa	aggtggacac	agctgctcag	accaatagcc	gcctggcccc	gcccacgagg	3600
ctgtccctgg	gggatcccaa	ggccagcacc	ttacctcggg	cccagagagca	gcagcagcag	3660
cagcagccct	tgtctcaccc	tccagagccc	aagagcccgg	gggaatatgt	caatattgaa	3720

```

tttgggagtg atcagtcctgg ctacttgtct gggccggtgg ctttccacag ctcaccttct 3780
gtcagggtgtc catcccagct ccagccagct cccagagagg aagagactgg cactgaggag 3840
tacatgaaga tggacctggg gccgggcccgg agggcagcct ggcaggagag cactgggggtc 3900
gagatgggca gactggggccc tgcacctccc ggggctgcta gcatttgag gcctacccgg 3960
gcagtgccca gcagccgggg tgactacatg accatgcaga tgagtgtcc ccgtcagagc 4020
tacgtggaca cctcgccagc tggccctgta agctatgctg acatgcgaac aggcattgct 4080
gcagaggagg tgagcctgcc cagggccacc atggctgctg cctcctcatc ctcagcagcc 4140
tctgcttccc cgactgggccc tcaaggggca gcagagctgg ctgcccactc gtccctgctg 4200
ggggggccac aaggacctgg gggcatgagc gccttcaccc gggagaacct cagtccaac 4260
cgcaaccaga gtgccaaagt gatccgtgca gaccacaag ggtgccggcg gaggcatagc 4320
tccgagactt tctcctcaac acccagtgcc acccgggtgg gcaacacagt gccctttgga 4380
gcggggggcag cagtaggggg cgggtggcgg agcagcagca gcagcgagga tgtgaaacgc 4440
cacagctctg cttcctttga gaatgtgtgg ctgaggcctg gggagcttgg gggagcccc 4500
aaggagccag ccaaactgtg tggggctgct gggggtttgg agaattgtct taactacata 4560
gacctggatt tgggtcaagga cttcaaacag tgccctcagg agtgcacccc tgaaccgcag 4620
cctccccac cccaccccc tcatcaaccc ctgggcagcg gtgagagcag ctccaccgcg 4680
cgctcaagtg aggatttaag cgcctatgcc agcatcagtt tccagaagca gccagaggac 4740
cgtcagtagc tcaactggac atcacagcag aatgaagacc taaatgacct cagcaaatcc 4800
tcttctaact catgggtacc cagactctaa atatttcag attcacaact aggacctcat 4860
atcttcctca tcagtagatg gtacgatgca tccatttcag tttgtttact ttatccaatc 4920
ctcaggattt cattgactga actgcacgtt ctatattgtg ccaagcgaaa aaaaaaatg 4980
cactgtgaca ccagaataat gagtctgcat aaacttcac ttcaacctta aggacttagc 5040
tggccacagt gagctgatgt gcccaccacc gtgtcatgag agaattgggtt tactctcaat 5100
gcattttcaa gatacatttc atctgctgct gaaactgtgt acgacaaagc atcattgtaa 5160
attatttcat acaaaactgt tcacgttggg tggagagagt attaaatatt taacataggt 5220
tttgatttat atgtgtaatt ttttaaataa aaatgtaact tttcttacag cacatctttt 5280
ttttggatgt gggatggagg tatacaatgt tctgttgtaa agagtggagc aaatgcttaa 5340
aacaaggctt aaaagagtag aataggggtat gatccttgtt ttaagattgt aattcagaaa 5400
acataatata agaatacatg tgccatagat ggttctcaat tgtatagtta ttttgctga 5460
tactatctct tgtcatataa acctgatgtt gagctgagtt ccttataaga attaatctta 5520
attttgtatt ttttctgta agacaatagg ccatgttaat taaactgaag aaggatatat 5580
ttggctgggt gttttcaaat gtcagcttaa aattggtaat tgaatggaag caaaattata 5640
agaagaggaa attaaagtct tccattgcat gtattgtaaa cagaaggaga tgggtgattc 5700
cttcaattca aaagctctct ttggaatgaa caatgtgggc gtttgtaaat tctggaaatg 5760
tctttctatt cataataaac tagatactgt tgatctttta aaaaaaaaaa aaaaaaaaaa 5820
aaaaaaaaa

```

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 7

Asp Tyr Lys Asp Asp Asp Lys

1

5

<210> 8
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 8
gggggaattt gtcaata 17

<210> 9
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 9
gaatttgтта atattg 16